

SEQUENCE LISTING

SEQ ID NO.1

SEQUENCE LENGTH: 556

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION

Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg  
1 5 10 15  
Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr  
20 25 30  
Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg  
35 40 45  
His Ile Ile Asp Asn Thr Ser Thr Lys Val Tyr Met Ala Glu Ile  
50 55 60  
Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile  
65 70 75 80  
Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala  
85 90 95  
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu  
100 105 110  
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu  
115 120 125  
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro  
130 135 140  
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr  
145 150 155 160  
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val  
165 170 175  
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu  
180 185 190  
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val  
195 200 205  
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr  
210 215 220

Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr  
 225 230 235 240  
 Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg  
 245 250 255  
 Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu  
 260 265 270  
 Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr  
 275 280 285  
 Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly  
 290 295 300  
 Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr  
 305 310 315 320  
 Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile  
 325 330 335  
 Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe  
 340 345 350  
 Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu  
 355 360 365  
 Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr  
 370 375 380  
 Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr  
 385 390 395 400  
 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg  
 405 410 415  
 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly  
 420 425 430  
 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr  
 435 440 445  
 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly  
 450 455 460  
 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met  
 465 470 475 480  
 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly  
 485 490 495  
 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln  
 500 505 510

Thr	Ser	Val	Ala	Asp	Pro	Thr	Ser	Lys	Val	His	Asn	Phe	Asn	Asn	Leu
515						520						525			
Trp	Val	Gly	Gly	Asn	Gly	Cys	Ile	Pro	Asp	Ala	Thr	Ala	Cys	Asn	Pro
530						535						540			
Thr	Arg	Thr	Ser	Val	Ala	Tyr	Ala	Leu	Lys	Gly	Ala	Glu	Ala	Val	Val
545						550						555			560
Asn	Tyr	Leu	Gly	Val	Ser	*									
						565									

## SEQ ID NO.2

SEQUENCE LENGTH: 1701

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to RNA

## SEQUENCE DESCRIPTION

ATG	CCG	ATA	CGT	CTT	TCC	AAA	GAA	AAA	ATC	AAC	GAC	CTG	CTG	CAA	CGT	48
Met	Pro	Ile	Arg	Leu	Ser	Lys	Glu	Lys	Ile	Asn	Asp	Leu	Leu	Gln	Arg	
1				5					10					15		
TCT	CAA	GGG	GAT	CTT	ACT	TCC	TCG	CAA	CAC	GAA	ATT	GTA	CAT	TTC	ACT	96
Ser	Gln	Gly	Asp	Leu	Thr	Ser	Ser	Gln	His	Glu	Ile	Val	His	Phe	Thr	
				20					25					30		
GAT	GTT	TTC	ATT	GCT	GGC	AGT	GGT	CCC	ATT	AGC	TGT	ACT	TAC	GCC	CGC	144
Asp	Val	Phe	Ile	Ala	Gly	Ser	Gly	Pro	Ile	Ser	Cys	Thr	Tyr	Ala	Arg	
				35				40						45		
CAC	ATC	ATT	GAC	AAT	ACC	TCA	ACT	ACA	AAG	GTT	TAC	ATG	GCC	GAA	ATA	192
His	Ile	Ile	Asp	Asn	Thr	Ser	Thr	Thr	Lys	Val	Tyr	Met	Ala	Glu	Ile	
				50				55						60		
GGT	TCT	CAA	GAT	AAC	CCT	GTC	ATC	GGG	GCC	CAT	CAC	AAG	AAC	TCC	ATA	240
Gly	Ser	Gln	Asp	Asn	Pro	Val	Ile	Gly	Ala	His	His	Lys	Asn	Ser	Ile	
				65			70							75	80	
AAG	TTT	CAG	AAA	GAC	ATT	GAC	AAG	TTT	GTG	AAT	ATC	ATC	AAC	GGT	GCC	288
Lys	Phe	Gln	Lys	Asp	Ile	Asp	Lys	Phe	Val	Asn	Ile	Ile	Asn	Gly	Ala	
				85				90						95		

CTC CAG CCG ATT TCG ATT TCG CCA TCG GAC ACC TAC CAG CCC ACT CTC	336
Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu	
100 105 110	
GCT GTA GCA GCG TGG GCG CCG CCC ATC GAT CCT GCC GAA GGC CAG CTC	384
Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu	
115 120 125	
GTG ATT ATG GGA CAC AAT CCG AAT CAG GAG GCC GGC CTG AAC CTT CCC	432
Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro	
130 135 140	
GGT AGC GCT GTC ACT AGG ACA GTC GGG GGG ATG GCG ACC CAC TGG ACT	480
Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr	
145 150 155 160	
TGC GCG TGT CCT ACT CCA CAT GAC GAA GAG AGG GTC AAC AAC CCA GTT	528
Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val	
165 170 175	
GAC AAG CAG GAG TTC GAC GCA CTG CTC GAA CGT GCT AAA ACA TTG CTC	576
Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu	
180 185 190	
AAC GTT CAC AGC GAC CAG TAC GAC GAT TCT ATC CGT CAG ATA GTT GTC	624
Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val	
195 200 205	
AAA GAG ACT CTT CAG CAG ACC CTT GAT GCG TCG CGG GGT GTG ACC ACT	672
Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr	
210 215 220	
CTC CCG CTG GGG GTG GAG CGC CGT ACG GAC AAT CCT ATT TAT GTC ACC	720
Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr	
225 230 235 240	
TGG ACC GGT GCC GAT ACC GTC CTT GGT GAT GTG CCG AAG AGT CCC CGA	768
Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg	
245 250 255	
TTC GCT TTG GTT ACA GAG ACG AGA GTG ACG AAG CTT ATT GTC AGT GAA	816
Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu	
260 265 270	
ACC AAT CCG ACG CAG GTT GTC GCG TTG CTA CGT AAC TTG AAT ACA	864
Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr	
275 280 285	

AGC AAC GAT GAA CTT GTC GTG GCC AAG AGT TTC GTC ATA GCT TGT GGA	912
Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly	
290 295 300	
GCA GTC TGC ACA CCG CAA ATC TTG TGG AAC AGC AAC ATC CGC CCA TAT	960
Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr	
305 310 315 320	
GCG CTT GGT CGC TAC CTC AGC GAA CAG TCC ATG ACT TTT TGT CAG ATC	1008
Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile	
325 330 335	
GTT CTC AAG AGG GGC ATA GTC GAT GCC ATC GCT ACT GAC CCT CGC TTC	1056
Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe	
340 345 350	
GCG AAG GTT GAG GCG CAC AAG AAG CAC CCC GAT GAC GTG CTG	1104
Ala Ala Lys Val Glu Ala His Lys Lys His Pro Asp Asp Val Leu	
355 360 365	
CCC ATT CCA TTC CAC GAG CCT GAA CCT CAA GTG ATG ATT CCG TAC ACG	1152
Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr	
370 375 380	
TCG GAC TTC CCT TGG CAT GTT CAG GTG CAT CGC GAT GCA TTC TCA TAT	1200
Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr	
385 390 395 400	
GGT GAT GTT GGA CCC AAG GCC GAC CCG CGT GTT GTC GTC GAT CTG AGG	1248
Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg	
405 410 415	
TTT TTC GGC AAA TCA GAT ATT GTC GAA GAA AAT CGA GTG ACT TTC GGT	1296
Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly	
420 425 430	
CCG AAC CCT AAG CTA CGC GAG TGG GAA GCG GGT GTT ACA GAC ACT TAT	1344
Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr	
435 440 445	
GGA ATG CCA CAG CCG ACA TTC CAT GTC AAG CGG ACC AAC GCC GAT GGA	1392
Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly	
450 455 460	
GAC CGT GAC CAG AGG ATG ATG AAT GAT ATG ACC AAC GTC GCG AAC ATG	1440
Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met	
465 470 475 480	

CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT	1488		
Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly			
485	490	495	
CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA	1536		
Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln			
500	505	510	
ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG	1584		
Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu			
515	520	525	
TGG GTC GGC GGG AAT GGG TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG	1632		
Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro			
530	535	540	
ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC	1680		
Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val			
545	550	555	560
AAT TAC CTT GGC GTC TCC TGA	1701		
Asn Tyr Leu Gly Val Ser *			
565			

SEQ ID NO.3

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser

1 5 10 15

Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His

20 25

SEQ ID NO.4

SEQUENCE LENGTH: 57

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser

1

5

10

15

Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr Asp

20

25

30

Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg His

35

40

45

Ile Ile Asp Asn Thr Ser Thr Thr Lys

50

55

SEQ ID NO.5

SEQUENCE LENGTH: 19

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val Tyr Met Ala Glu Ile Gly Ser Gln Asp Asn Pro Val Ile Gly Ala

1

5

10

15

His His Lys

SEQ ID NO.6

SEQUENCE LENGTH: 61

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Phe Val Asn Ile Ile Asn Gly Ala Leu Gln Pro Ile Ser Ile Ser Pro

1

5

10

15

Ser Asp Thr Tyr Gln Pro Thr Leu Ala Val Ala Ala Trp Ala Pro Pro

20

25

30

Ile Asp Pro Ala Glu Gly Gln Leu Val Ile Met Gly His Asn Pro Asn

35

40

45

Gln Glu Ala Gly Leu Asn Leu Pro Gly Ser Ala Val Thr

50

55

60

SEQ ID NO.7

SEQUENCE LENGTH: 29

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Arg Thr Val Gly Gly Met Ala Thr His Trp Thr Cys Ala Cys Pro Thr

1

5

10

15

Pro His Asp Glu Glu Arg Val Asn Asn Pro Val Asp Lys

20

25

SEQ ID NO.8

SEQUENCE LENGTH: 31

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu Asn Val

1 5 10 15

His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val Lys

20 25 30

SEQ ID NO.9

SEQUENCE LENGTH: 58

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr Leu

1 5 10 15

Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr Trp

20 25 30

Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg Phe

35 40 45

Ala Leu Val Thr Glu Thr Arg Val Thr Lys

50 55

SEQ ID NO.10

SEQUENCE LENGTH: 30

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Leu Ile Val Ser Glu Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu  
1 5 10 15  
Arg Asn Leu Asn Thr Ser Asn Asp Glu Leu Val Val Ala Lys  
20 25 30

SEQ ID NO.11

SEQUENCE LENGTH: 58

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Ser Phe Val Ile Ala Cys Gly Ala Val Cys Thr Pro Gln Ile Leu Trp  
1 5 10 15  
Asn Ser Asn Ile Arg Pro Tyr Ala Leu Gly Arg Tyr Leu Ser Glu Gln  
20 25 30  
Ser Met Thr Phe Cys Gln Ile Val Leu Lys Arg Gly Ile Val Asp Ala  
35 40 45  
Ile Ala Thr Asp Pro Arg Phe Ala Ala Lys  
50 55

SEQ ID NO.12

SEQUENCE LENGTH: 51

SEQUENCE TYPE: amino acid

STRANNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu Pro Ile Pro

1 5 10 15

Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr Ser Asp Phe

20 25 30

Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr Gly Asp Val

35 40 45

Gly Pro Lys

50

SEQ ID NO.13

SEQUENCE LENGTH: 30

SEQUENCE TYPE: amino acid

STRANNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Ala Asp Pro Arg Val Val Val Asp Leu Arg Phe Phe Gly Lys Ser Asp

1 5 10 15

Ile Val Glu Glu Asn Arg Val Thr Phe Gly Pro Asn Pro Lys

20 25 30

SEQ ID NO.14

SEQUENCE LENGTH: 50

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr Gly Met Pro Gln

1 5 10 15

Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly Asp Arg Asp Gln

20 25 30

Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met Leu Gly Gly Tyr

30 40 45

Leu Pro

50

SEQ ID NO.15

SEQUENCE LENGTH: 35

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly Leu Val Leu His Ile Thr

1 5 10 15

Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln Thr Ser Val Ala Asp Pro

20 25 30

Thr Ser Lys

35

SEQ ID NO.16

SEQUENCE LENGTH: 33

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Val His Asn Phe Asn Asn Leu Trp Val Gly Gly Asn Gly Cys Ile Pro

1

5

10

15

Asp Ala Thr Ala Cys Asn Pro Thr Arg Thr Ser Val Ala Tyr Ala Leu

20

25

30

Lys

SEQ ID NO.17

SEQUENCE LENGTH: 12

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Gly Ala Glu Ala Val Val Asn Tyr Leu Gly Val Ser

1

5

10

SEQ ID NO.18

SEQUENCE LENGTH: 22

SEQUENCE TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Asn Ser Ile Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile

1

5

10

15

Asn Gly Ala Leu Gln Pro

20

SEQ ID NO.19

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGACCAT GGGGTATCGT CTTTCC

26

SEQ ID NO.20

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SEQUENCE DESCRIPTION

GAGAGAGGGAT CCGGAGACGC CAAGGAT

27